

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hermeking, Heiko
Vogelstein, Bert
Kinzler, Kenneth
- (ii) TITLE OF THE INVENTION: 14-3-3 SIGMA ARREST THE CELL
CYCLE
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Banner & Witcoff
(B) STREET: 1001 G Street, NW
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20001
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 18-DEC-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Kagan, Sarah A
(B) REGISTRATION NUMBER: 32141
(C) REFERENCE/DOCKET NUMBER: 1107.72886
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-508-9100
(B) TELEFAX: 202-508-9299
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAGAGACACA	GAGTCCGGCA	TTGGTCCCAG	GCAGCAGTTA	GCCCGCCGCC	CGCCTGTGTG	60
TCCCCAGAGC	CATGGAGAGA	GCCAGTCTGA	TCCAGAAGGC	CAAGCTGGCA	GAGCAGGCCG	120
AACGCTATGA	GGACATGGCA	GCCTTCATGA	AAGGCGCCGT	GGAGAAGGGC	GAGGAGCTCT	180
CCTGCGAAGA	GCGAAACCTG	CTCTCAGTAG	CCTATAAGAA	CGTGGTGGGC	GGCCAGAGGG	240
CTGCCTGGAG	GGTGTGTGCC	AGTATTGAGC	AGAAAAGCAA	CGAGGAGGGC	TCGGAGGAGA	300
AGGGGCCCCG	GGTGCCTGAG	TACCGGGAGA	AGGTGGAGAC	TGAGCTCCAG	GGCGTGTGCG	360
ACACCGTGCT	GGGCCTGCTG	GACAGCCACC	TCATCAAGGA	GGCCGGGGAC	GCCGAGAGCC	420
GGGTCTTCTA	CCTGAAGATG	AAGGGTGA	ACTACCGCTA	CCTGGCCGAG	GTGGCCACCG	480
GTGACGACAA	GAAGCGCATC	ATTGACTCAG	CCCGGTCAGC	CTACCAGGAG	GCCATGGACA	540
TCAGCAAGAA	GGAGATGCCG	CCCACCAACC	CCATCCGCCT	GGGCCTGGCC	CTGAACTTTT	600
CCGTCTTCCA	CTACGAGATC	GCCAACAGCC	CCGAGGAGGC	CATCTCTCTG	GCCAAGACCA	660
CTTTCGACGA	GGCCATGGCT	GATCTGCACA	CCCTCAGCGA	GGACTCCTAC	AAAGACAGCA	720
CCCTCATCAT	GCAGCTGCTG	CGAGACAACC	TGACACTGTG	GACGGCCGAC	AACGCCGGGG	780
AAGAGGGGGG	CGAGGCTCCC	CAGGAGCCCC	AGAGCTGAGT	GTTGCCCGCC	ACCGCCCCGC	840
CCTGCCCCCT	CCAGTCCCCC	ACCCTGCCGA	GAGGACTAGT	ATGGGGTGGG	AGGCCCCACC	900
CTTCTCCCCCT	AGGCGCTGTT	CTTGCTCCAA	AGGGCTCCGT	GGAGAGGGAC	TGGCAGAGCT	960
GAGGCCACCT	GGGGCTGGGG	ATCCCACTCT	TCTTGACAGT	GTTGAGCGCA	CCTAACCACCT	1020
GGTCATGCCC	CCACCCCTGC	TCTCCGCACC	CGCTTCCTCC	CGACCCCAAG	ACCAGGCTAC	1080
TTCTCCCCTC	CTCTTGCCCTC	CCTCCTGCCC	CTGCTGCCTC	TGATCGTAGG	AATTGAGGAG	1140
TGTCCCGCCT	TGTGGCTGAG	AACTGGACAG	TGGCAGGGGC	TGGAGATGGG	TGTGTGTGTG	1200
TGTGTGTGTG	TGTGTGTGTG	CGCGCGCGCC	AGTGCAAGAC	CGAGACTGAG	GGAAAGCATG	1260
TCTGCTGGGT	GTGACCATGT	TTCCTCTCAA	TAAAGTTCCC	CTGTGACACT	CAAAAAAAAA	1320

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Arg	Ala	Ser	Leu	Ile	Gln	Lys	Ala	Lys	Leu	Ala	Glu	Gln	Ala
1				5				10					15		
Glu	Arg	Tyr	Glu	Asp	Met	Ala	Ala	Phe	Met	Lys	Gly	Ala	Val	Glu	Lys
			20					25					30		
Gly	Glu	Glu	Leu	Ser	Cys	Glu	Glu	Arg	Asn	Leu	Leu	Ser	Val	Ala	Tyr
		35					40					45			

Lys Asn Val Val Gly Gly Gln Arg Ala Ala Trp Arg Val Leu Ser Ser
 50 55 60
 Ile Glu Gln Lys Ser Asn Glu Glu Gly Ser Glu Glu Lys Gly Pro Glu
 65 70 75 80
 Val Arg Glu Tyr Arg Glu Lys Val Glu Thr Glu Leu Gln Gly Val Cys
 85 90 95
 Asp Thr Val Leu Gly Leu Leu Asp Ser His Leu Ile Lys Glu Ala Gly
 100 105 110
 Asp Ala Glu Ser Arg Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr Tyr
 115 120 125
 Arg Tyr Leu Ala Glu Val Ala Thr Gly Asp Asp Lys Lys Arg Ile Ile
 130 135 140
 Asp Ser Ala Arg Ser Ala Tyr Gln Glu Ala Met Asp Ile Ser Lys Lys
 145 150 155 160
 Glu Met Pro Pro Thr Asn Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe
 165 170 175
 Ser Val Phe His Tyr Glu Ile Ala Asn Ser Pro Glu Glu Ala Ile Ser
 180 185 190
 Leu Ala Lys Thr Thr Phe Asp Glu Ala Met Ala Asp Leu His Thr Leu
 195 200 205
 Ser Glu Asp Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg
 210 215 220
 Asp Asn Leu Thr Leu Trp Thr Ala Asp Asn Ala Gly Glu Glu Gly Gly
 225 230 235 240
 Glu Ala Pro Gln Glu Pro Gln Ser
 245

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATCCCAGC	CTGCCCCCTCC	ACTTCTCTCC	CAAGCCAGGT	CCCGGCATGG	GTGGGTTATG	60
CTCATGCTGG	CAATACTTGA	AACGGGTTTA	TTAATGCTGG	GTATTTTGCA	CAATTTTATA	120
GACCTCTTTT	CTACATAGTC	TTTTTTAAAT	GGAAGGAGAA	AATGTCAGCC	ACATTACTGT	180
CTGTGTAGTG	CCAGGTGAAG	GGTTATCAGA	AGGCTGGTTG	GTTTTAATAA	GTTTATTCCA	240
AGAGACCTTC	TGGCTGGAAT	GAGTGAGAGT	GTGTGTGCAT	GTGTGTGTGT	GTTTCATGTGT	300
GCCCTGTATG	AATGTGGCTG	GCTCCCAGAT	CCCCTGGGCT	GCCCCCTGCC	CCATCCCCTT	360
TGAGTATCAG	AAGCACTCTG	AGCCAAGGGG	ACAGGGGGCA	CGTGCACTGG	TCACGAGAAA	420
ACCTTGGGCT	CCCACTGGGG	CTCAGCCCAG	CCTCCTATCT	TTCCTTCTTC	TATGGACTTC	480
AGACAGCCAG	TGTCTGGGGA	CTCTGCCACT	CTACCCCCAG	CCCTACCCAC	CAGCCCCCAG	540
GTGAGGCTTC	CAGCTGGGAC	CTGCCCAGAC	AGGCTGAGCC	TGGGCGTGGT	GGGTGGGGTG	600
ATGGCTCTGG	GGAGCGGCTG	CCATCCTACA	AGCCACACCC	CCTCCTCTGA	GCTCTGAATA	660
TGGGACCCAG	TGCCAGGAGC	TGGAAGACAA	GGTGTTCCTG	CCAAACGGGA	CCTCCATCCA	720
GAGAAAAGGA	AGAAGGTGCA	GGGTGGGCCA	AGAGGCAAGT	GAAGGTTGGC	CTGAGTCTGG	780
GCCGGAAACT	CAGAGGATGT	TTCTCCTCTG	CTGGGAGCTG	TAGTTTCTTA	TCAAAATAGA	840

AGCAGGGAAA	GAACGTTGGC	AACAGAGGTC	TCCATCTCTG	AGGACTCTGC	CAGGGGTCAG	7140
AGATGGGGCA	ATGGTCAAAA	GGAAGGAACA	GGCCAGGCAC	AGTGGCTCAT	GCCCATAATC	7200
CCAGCACTTT	GGGAGGCTGA	GGCAGGAGGA	TCGCTTGAGC	CCAGGAGTTT	GAGACCTGCC	7260
TGGGCAATGT	AGTGAGATCT	GCTCTCTATT	TAAAAAAAAA	AAAAAGGAAA	GAACAAGTAA	7320
ACTTCTGAGA	AACAGGCTGG	GGGAGGCATC	ACGTAGCTGG	AATTGCTGCC	CCATAAAACA	7380
GAATGGTATG	TGTCAGTGCC	ACCTCCCTTT	CTCAGTCCTC	TCTCTCCCCA	GGTTGCTAGC	7440
GTCCCCCTGG	GGGATCAAAC	TGGACTGCTT	CCCAGCCTCA	GACAGAGAGC	AGTCTGAGTC	7500
AGGCAGGAAA	GTGGGACAGC	CGGGGAGCTG	GACCCACCCC	TCTGTGAGCC	CCGCTGGTAC	7560
CTGATGGCAT	GTGGCTTGGA	GAGGGCAGGT	GACCTGGCGT	GGAGGGCCAG	AGGGTAAATC	7620
CTCAAACAAG	TGGCAACAGG	CCACCAACTT	GAAAGGGAAA	ATTGTGTAGT	GATGGGAAAT	7680

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGCATGTGC CACCATGCCC

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTAGCATTAG CCCAGACATG TCC

23